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(D) analyzing the interaction of all or part of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

30. (Once Amended) A method according to claim 29, 51, or 52 wherein said analyzing step comprises a DEE computation.

31. (Once Amended) A method according to claim 28, 29, 51 or 52 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.

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33. (Once Amended) A method according to claim 28, 29, 51 or 52 wherein said analyzing step includes the use of at least one scoring function.

34. (Once Amended) A method according to claim 33 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

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39. (Once Amended) A method according to claim 28, 29, 51 or 52 further comprising experimentally testing at least one member of said set.

40. (Once Amended) A method according to claim 31 further comprising the step of: generating a list of additional optimal sequences from said globally optimal protein sequence.

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42. (Once Amended) A method according to claim 29, 51 or 52 wherein said analyzing step comprises a Monte Carlo computation.

43. (Once Amended) A method according to claim 40 further comprising the step of: testing some or all of said protein sequences from said list to produce potential energy test results.

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45. (Once Amended) A recombinant protein comprising an optimized protein sequence generated by the method of claim 28, 29, 51, 52, 53 or 56.

**Please add the following claims.**

51. (New) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving a protein backbone structure with variable residue positions;
- (B) establishing a group of potential amino acids for each of said variable residue

positions; and

(C) analyzing the interaction of all or part of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized proteins sequences.

52. (New) A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving a protein backbone structure with variable residue positions;
- (B) establishing a group of potential amino acids for each of said variable residue

positions, wherein the group of potential amino acids for at least one of said variable residue positions has an amino acid selected from each of at least two different amino acids; and

(C) analyzing the interaction of all or part of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

**REMARKS**

Claims 28-48 are pending in this application. Claims 2-27, 49 and 50 have been cancelled. Claims 51 and 52 have been added. Support for added Claims 51 and 52 may be found in original claims 28 and 29 and in the Specification at page 5, lines 25-28 and page 6, lines 5-17. No new matter has been added by the amendments made to the claims. An Appendix of Pending Claims is attached for the Examiner's convenience.

**Rejection under 35 U.S.C. § 112, second paragraph**

Claims 2-20, 27-48 and 50 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. Without admitting the propriety of the rejection and reserving the right to pursue these claims at a later date, Claims 2-20, 27, and 50 have been cancelled making moot the rejection as applied to these claims. Claims 28-48 have been amended. Applicants respectfully request withdrawal of the rejection.